

Complete genome sequence of *Thermobispora bispora* type strain (R51^T)

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Thermobispora bispora (Henssen 1957) Wang et al. 1996 is the type species of the genus *Thermobispora*. This genus is of great interest because it is strictly thermophilic and because it has been shown for several of its members that the genome contains substantially distinct (6.4% sequence difference) and transcriptionally active 16S rRNA genes. Here we describe the features of this organism, together with the complete genome sequence and annotation. This is the second completed genome sequence of a member from the suborder *Streptosporangineae* and the first genome sequence of a member of the genus *Thermobispora*. The 4,189,976 bp long genome with its 3,596 protein-coding and 63 RNA genes is part of the *Genomic Encyclopedia of Bacteria and Archaea* project.

Introduction

Strain R51^T (= DSM 43833 = ATCC 19993 = JCM 10125) is the type strain of the species *Thermobispora bispora*, which is the type species of the genus *Thermobispora* [1]. The generic name of the genus derives from the Greek words ‘thermos’, ‘bis’, and ‘spora’, to indicate high temperature two-spored organisms [1]. Strain R51^T was isolated from decaying manure in Berlin (Germany) in 1954 [2]. Other strains were isolated during the same research project from other types of manure in other cities in Germany and in Finland

[2]. As deduced from 16S gene sequences, *T. bispora* was also found in compost in Sweden [3]. Historically, strain R51^T was originally classified in 1957 as *Thermopolyspora bispora* [2]. At the same time, a morphologically similar genus, *Microbispora*, was described [4], which has priority and *T. bispora* was subsequently transferred to the genus *Microbispora* [5,6]. However, based on thermal preferences [2,7], chemotaxonomic features [7], and the two-dimensional polyacrylamide gel electrophoresis patterns of the ribo-

somal protein AT-L30 [8], *Microbispora bispora* was subsequently removed from the genus *Microbispora* to be the type species of the new genus *Thermobispora* [1]. *T. bispora* is currently the only species in the genus *Thermobispora* [1]. In 1997 *T. bispora* gained interest, as it was described as the first organism to have two distinct (6.4% of total nucleotides) types of transcriptionally active 16S rRNA genes (GenBank accessions U83909 and U83912) [9]. Based on the two copies of the 16S rRNA genes that match best to sequence U83909 the closest related type strain (9% sequence difference [10]) is *Micromonospora pattaloongensis* [11] of the family *Micromonosporaceae*; based on the two copies of the 16S rRNA genes that match best to sequence U83912 the closest related type strain (8% sequence difference [10]) is *Planotetraspora silvatica* [12] of the family *Streptosporangiaceae*. Neither fit to the taxonomic position as shown in the List of Procarvotic names with Standing in Nomenclature that shows the genus *Thermobispora* as a member of the family *Pseudonocardiaceae*, reflecting the current uncertainty of the taxonomic position of *T. bispora* [13]. In their recent review of *Actinobacteria* taxonomy, Zhi *et al.* [14] suggested to

place *Thermobispora* in the suborder *Streptosporangineae* without assignment to a family, which is in accordance with our SSU rRNA tree (Figure 1). 16S rRNA sequences from environmental samples and metagenomic surveys with both 16S rRNA sequences detected phylotypes with approximately 89-92% 16S rRNA gene sequence similarity to both (U83909 and U83912) reference sequences only in a compost metagenome [21], indicating a very rare occurrence of *Thermobispora*-spp. in the environment (status March 2010). Here we present a summary classification and a set of features for *T. bispora* R51^T, together with the description of the complete genomic sequencing and annotation.

Classification and features

Figure 1 shows the phylogenetic neighborhood of for *T. bispora* R51^T in a 16S rRNA based tree. The sequences of the four 16S rRNA gene copies in the genome differ from each other by up to 94 nucleotides, and differ by up to 95 nucleotides from the previously published 16S rRNA sequence generated from ATCC 19993 (U58523).

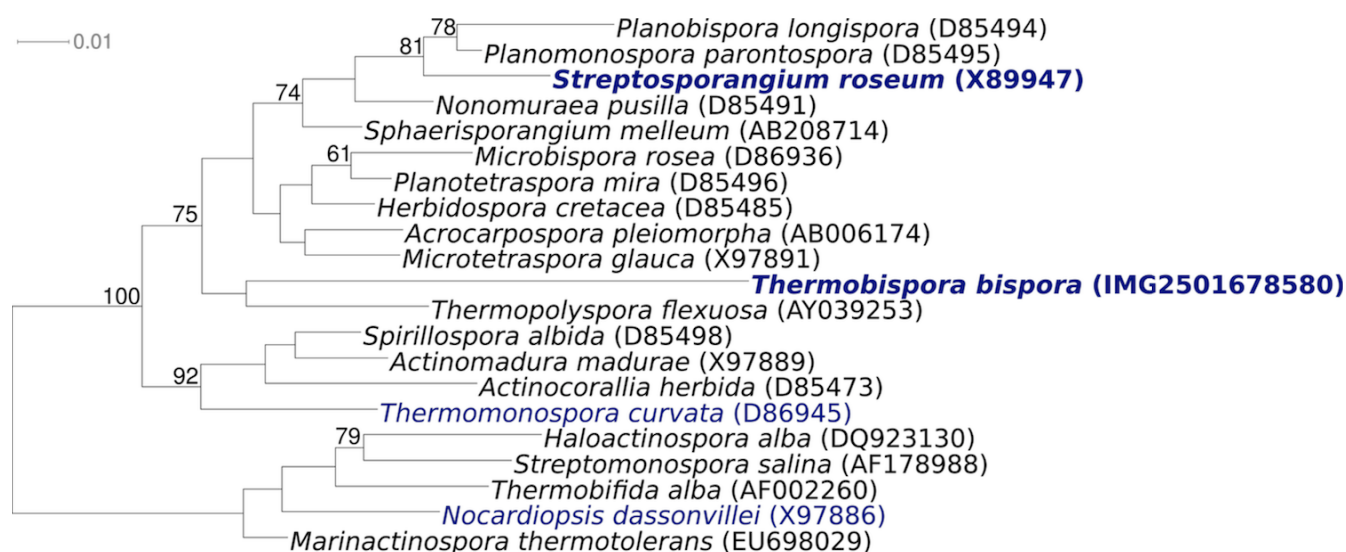


Figure 1. Phylogenetic tree highlighting the position of *T. bispora* R51^T relative to the type strains of the other genera within the suborder *Streptosporangineae* (except for *Actinoallomurus*, which was published after the analysis was completed). The tree was inferred from 1,371 aligned characters [15,16] of the 16S rRNA gene sequence under the maximum likelihood criterion [17] and rooted in accordance with the current taxonomy [18]. The branches are scaled in terms of the expected number of substitutions per site. Numbers above branches are support values from 1,000 bootstrap replicates if larger than 60%. Lineages with type strain genome sequencing projects registered in GOLD [19] are shown in blue, published genomes in bold, e.g. the recently published GEBA genome from *Streptosporangium roseum* [20].

T. bispora cells form substrate mycelia whose hyphae are 0.5 to 0.8 μm in diameter [1] (Figure 2). The aerial mycelia branch monopodally and bear longitudinal pairs of spores [1] (not visible in Figure 2). The spore diameters are usually 1.2 to 2.0 μm , but in liquid media spores with a diameter of 3 μm may occur [1]. The aerial mycelia are white, and the substrate mycelia are yellow or yellowish brown on the media used in the respective study (International *Streptomyces* Project medium 4 agar and IF0328 agar; Institute for Fermentation) [1]. No soluble pigment is produced [1]. *T. bispora* is an obligately thermophilic organism (Table 1) [1]. Starch is not hydrolyzed; inositol and rhamnose are utilized for growth, but arabinose and glycerol are not utilized [1]. Also, *T. bispora* is negative for iodinin production and nitrate reduction [1].

Chemotaxonomy

The cell wall of strain R51^T contains predominantly the menaquinone MK-9(H₀) (75%) and only small amounts of MK-9(H₂) and MK-9(H₄) [7]. Strain R51^T has a type PIV phospholipid pattern, and contains phosphatidylethanolamine but not

phosphatidylglycerol and trace amounts of glucosamine-containing phospholipids [7]. The cell wall contains a major amount of *meso*-diaminopimelic acid, and the whole-cell hydrolysate contains mannose and galactose [1]. The fatty acid composition of strain R51^T is dominated by saturated acids, with iso-C_{16:0} (55%) being the most frequent acid, followed by anteiso-C_{17:0} (8%), the unsaturated C_{18:1} (8%), iso-C_{18:0} (6%) and C_{16:0} [7]. Also, strain R51^T contains minor amounts of 10-methyl-branched chain fatty acids [7].

Genome sequencing and annotation

Genome project history

This organism was selected for sequencing on the basis of its phylogenetic position [27], and is part of the *Genomic Encyclopedia of Bacteria and Archaea* project [28]. The genome project is deposited in the Genome OnLine Database [19] and the complete genome sequence is deposited in GenBank. Sequencing, finishing and annotation were performed by the DOE Joint Genome Institute (JGI). A summary of the project information is shown in Table 2.

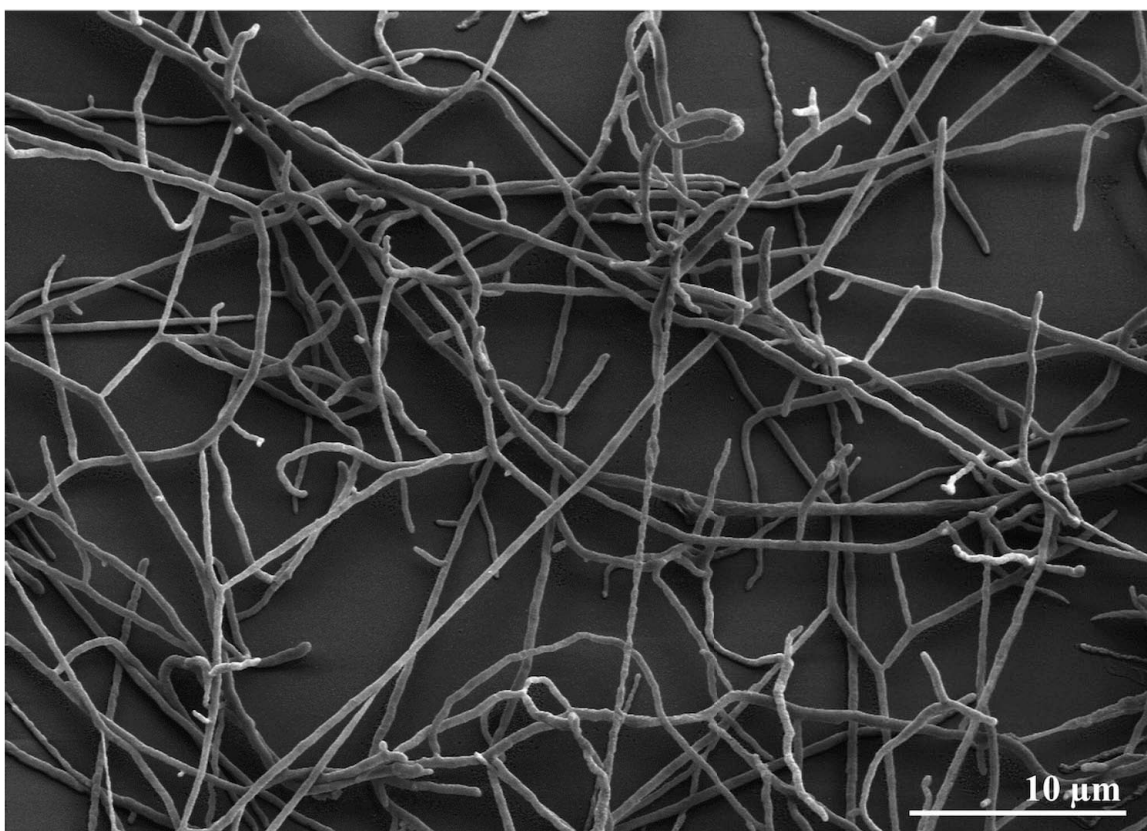


Figure 2. Scanning electron micrograph of *T. bispora* R51^T

Table 1. Classification and general features of *T. bispora* R51^T according to the MIGS recommendations [22]

MIGS ID	Property	Term	Evidence code
		Domain <i>Bacteria</i>	TAS [23]
		Phylum ' <i>Actinobacteria</i> '	TAS [13]
		Class <i>Actinobacteria</i>	TAS [24]
		Subclass <i>Actinobacteridae</i>	TAS [14,24]
	Current classification	Order <i>Actinomycetales</i>	TAS [14]
		Suborder <i>Streptosporangineae</i>	TAS [14]
		Family Incertae sedis	TAS [14]
		Genus <i>Thermobispora</i>	TAS [1]
		Species <i>Thermobispora bispora</i>	TAS [2]
		Type strain R51	TAS [5]
	Gram stain	positive	TAS [1]
	Cell shape	mycelia with hyphae	TAS [2]
	Motility	non-motile	TAS [1]
	Sporulation	sporulating	TAS [1]
	Temperature range	thermophile, 50°C - 65°C	TAS [1]
	Optimum temperature	not determined	TAS [1]
	Salinity	not determined	TAS [1]
MIGS-22	Oxygen requirement	aerobic	TAS [1,2]
	Carbon source	inositol and rhamnose	TAS [1]
	Energy source	sugars	TAS [1]
MIGS-6	Habitat	compost and other decaying material	TAS [2,3]
MIGS-15	Biotic relationship	unknown	
MIGS-14	Pathogenicity	not reported	
	Biosafety level	1	TAS [25]
	Isolation	decaying mixed manure	TAS [2]
MIGS-4	Geographic location	Berlin, Germany	TAS [2]
MIGS-5	Sample collection time	September 30, 1954	TAS [2]
MIGS-4.1	Latitude	52.52	NAS
MIGS-4.2	Longitude	14.42	
MIGS-4.3	Depth	not reported	
MIGS-4.4	Altitude	not reported	

Evidence codes - IDA: Inferred from Direct Assay (first time in publication); TAS: Traceable Author Statement (i.e., a direct report exists in the literature); NAS: Non-traceable Author Statement (i.e., not directly observed for the living, isolated sample, but based on a generally accepted property for the species, or anecdotal evidence). These evidence codes are from of the Gene Ontology project [26]. If the evidence code is IDA, then the property was directly observed for a live isolate by one of the authors or an expert mentioned in the acknowledgements.

Growth conditions and DNA isolation

T. bispora strain R51^T, DSM 43833, was grown in DSMZ medium 84 (Rolled oats mineral medium) [29] at 55°C. DNA was isolated from 1-1.5 g of cell paste using Qiagen Genomic 500 DNA Kit (Qiagen, Hilden, Germany) with lysis modification st/FT according to Wu *et al.* [28].

Genome sequencing and assembly

The genome of *T. bispora* was sequenced using a combination of Sanger and 454 sequencing platforms. All general aspects of library construction and sequencing can be found at <http://www.jgi.doe.gov/>. 454 pyrosequencing reads were assembled using the Newbler assembler version 1.1.02.15 (Roche). Large Newbler contigs were broken into 4,798

overlapping fragments of 1,000 bp and entered into assembly as pseudo-reads. The sequences were assigned quality scores based on Newbler consensus q-scores with modifications to account for overlap redundancy and to adjust inflated q-scores. A hybrid 454/Sanger assembly was made using the parallel phrap assembler (High Performance Software, LLC). Possible mis-assemblies were corrected with Dupfinisher or transposon bombing of bridging clones [30]. Gaps between

contigs were closed by editing in Consed, custom primer walk or PCR amplification. A total of 1,181 Sanger finishing reads were produced to close gaps, to resolve repetitive regions, and to raise the quality of the finished sequence. The error rate of the completed genome sequence is less than 1 in 100,000. The final assembly consists of 40,290 Sanger and 1.1× pyrosequence based pseudo-reads. Together Sanger reads and pseudo-reads provided 8.19× coverage of the genome.

Table 2. Genome sequencing project information

MIGS ID	Property	Term
MIGS-31	Finishing quality	Finished
	Libraries used	Three genomic libraries: two Sanger libraries – 8 kb pMCL200 and fosmid pcc1FOS and one 454 pyrosequence standard library
MIGS-28		
MIGS-29	Sequencing platforms	ABI3730, 454 GS FLX
MIGS-31.2	Sequencing coverage	7.1× Sanger; 1.1× pyrosequence pseudo-reads
MIGS-30	Assemblers	Newbler version 1.1.02.15, phrap
MIGS-32	Gene calling method	Prodigal, GenePRIMP
	INSDC ID	CP001874
	Genbank Date of Release	May 17, 2010
	GOLD ID	Gc01281
	NCBI project ID	469371
	Database: IMG-GEBA	2501651196
MIGS-13	Source material identifier	DSM 43833
	Project relevance	Tree of Life, GEBA

Table 3. Genome Statistics

Attribute	Value	% of Total
Genome size (bp)	4,189,976	100.00%
DNA coding region (bp)	3,548,135	84.68%
DNA G+C content (bp)	3,034,765	72.43%
Number of replicons	1	
Extrachromosomal elements	0	
Total genes	3,659	100.00%
RNA genes	63	1.72%
rRNA operons	3	
Protein-coding genes	3,596	98.28%
Pseudo genes	50	1.37%
Genes with function prediction	2,632	71.93%
Genes in paralog clusters	491	13.42%
Genes assigned to COGs	2,610	71.33%
Genes assigned Pfam domains	2,844	77.73%
Genes with signal peptides	795	21.73%
Genes with transmembrane helices	864	23.61%
CRISPR repeats	6	

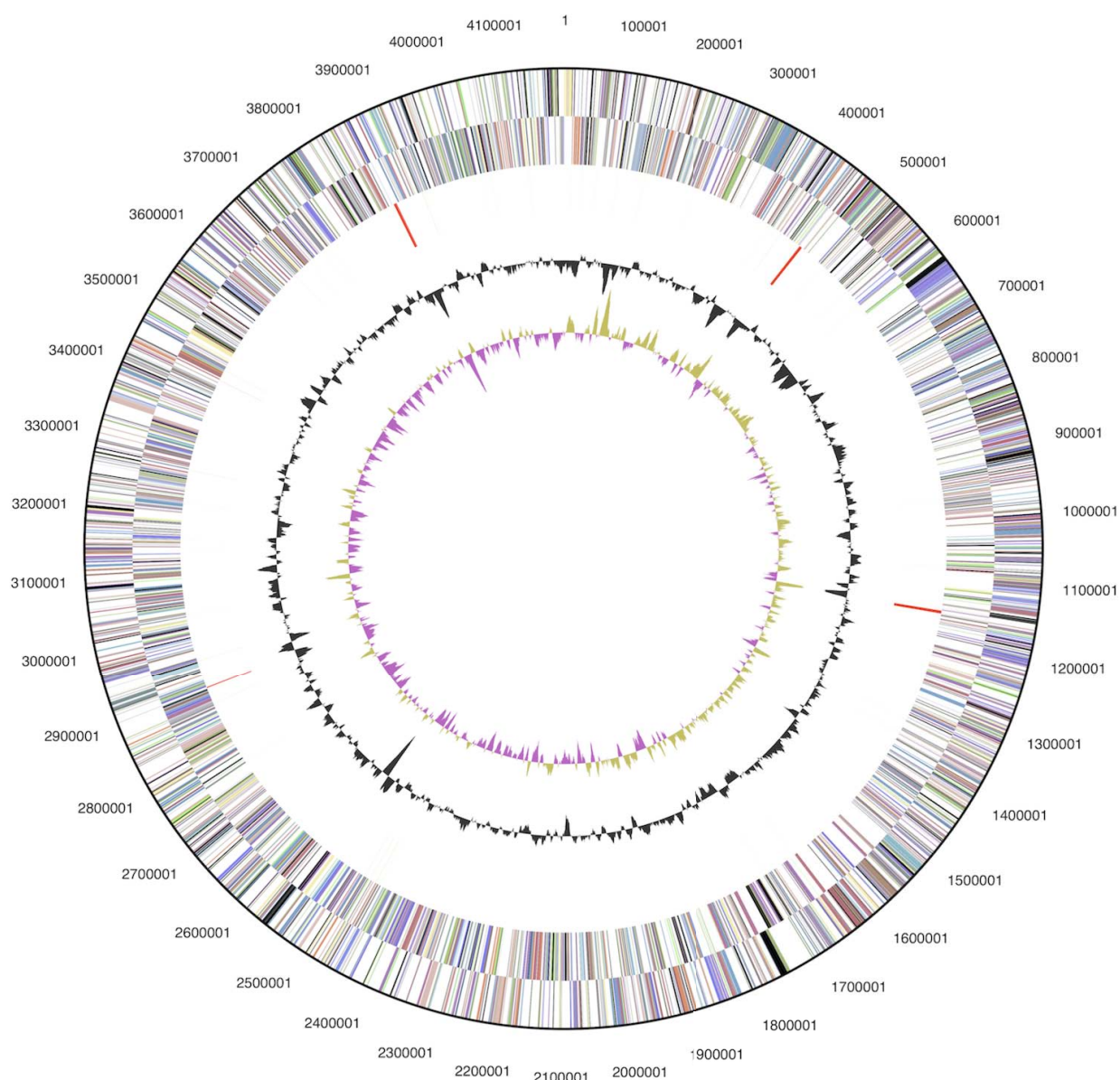


Figure 3. Graphical circular map of the genome. From outside to the center: Genes on forward strand (color by COG categories), Genes on reverse strand (color by COG categories), RNA genes (tRNAs green, rRNAs red, other RNAs black), GC content, GC skew.

Genome annotation

Genes were identified using [Prodigal](#) [31] as part of the Oak Ridge National Laboratory genome annotation pipeline, followed by a round of manual curation using the JGI [GenePRIMP](#) pipeline [32]. The predicted CDSs were translated and used to search the National Center for Biotechnology Information (NCBI) nonredundant database, UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. Additional gene prediction analysis and manual functional annotation was performed within the Integrated Microbial Genomes Expert Review (IMG-ER) platform [33].

Genome properties

The genome is 4,189,976 bp long and comprises one main circular chromosome with an overall GC content of 72.4% (Table 3 and Figure 3). Of the 3,659 genes predicted, 3,596 were protein-coding genes, and 63 RNAs; fifty pseudogenes were also identified. The majority of the protein-coding genes (71.9%) were assigned with a putative function while the remaining ones were annotated as hypothetical proteins. The distribution of genes into COGs functional categories is presented in Table 4.

Table 4. Number of genes associated with the general COG functional categories

Code	value	%age	Description
J	149	5.0	Translation, ribosomal structure and biogenesis
A	1	0.0	RNA processing and modification
K	304	10.3	Transcription
L	141	4.8	Replication, recombination and repair
B	1	0.0	Chromatin structure and dynamics
D	21	1.0	Cell cycle control, cell division, chromosome partitioning
Y	0	0.0	Nuclear structure
V	48	1.6	Defense mechanisms
T	192	6.5	Signal transduction mechanisms
M	140	4.7	Cell wall/membrane biogenesis
N	3	0.1	Cell motility
Z	0	0.0	Cytoskeleton
W	0	0.0	Extracellular structures
U	29	1.0	Intracellular trafficking, secretion, and vesicular transport
O	98	3.3	Posttranslational modification, protein turnover, chaperones
C	204	6.9	Energy production and conversion
G	221	7.5	Carbohydrate transport and metabolism
E	279	9.4	Amino acid transport and metabolism
F	82	2.8	Nucleotide transport and metabolism
H	146	4.9	Coenzyme transport and metabolism
I	133	4.5	Lipid transport and metabolism
P	138	4.7	Inorganic ion transport and metabolism
Q	85	2.9	Secondary metabolites biosynthesis, transport and catabolism
R	351	11.9	General function prediction only
S	191	6.5	Function unknown
-	1,049	28.7	Not in COGs

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